

This page gives you Search Results detail for the Application 10650507 and Search Result us-10-650-507-8.rag.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:09:29 ; Search time 200 Seconds
(without alignments)
1483.667 Million cell updates/sec

Title: US-10-650-507-8
Perfect score: 3518
Sequence: 1 MQQDGLGVGTRNGSGKGKRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	3518	100.0	649	2 AAY14541	Aay14541 Human lip
2	3518	100.0	649	3 AAY95822	Aay95822 Human lip
3	3518	100.0	649	4 AAB59901	Aab59901 Human lep
4	3507.5	99.7	650	8 ADP46576	Adp46576 Human col
5	3401.5	96.7	630	2 AAY14542	Aay14542 Human lip
6	3401.5	96.7	630	3 AAY95823	Aay95823 Human lip

7	3401.5	96.7	630	4	AAB59902	Aab59902	Human lep
8	3372.5	95.9	630	8	ADR08703	Adr08703	Human pro
9	3169	90.1	591	5	ABP68616	Abp68616	Human pan
10	3169	90.1	591	9	ADY15926	Ady15926	PRO polyp
11	3169	90.1	591	9	ADY20195	Ady20195	PRO polyp
12	3121	88.7	583	4	AAB88476	Aab88476	Human mem
13	3121	88.7	583	9	ADY63313	Ady63313	Human clo
14	3058	86.9	581	2	AAY14543	Aay14543	Human lip
15	3058	86.9	581	3	AAY95824	Aay95824	Human lip
16	3058	86.9	581	4	AAB59903	Aab59903	Human lep
17	2568	73.0	593	2	AAY14538	Aay14538	Rat lipol
18	2568	73.0	593	4	AAB59904	Aab59904	Rat lepti
19	2519.5	71.6	594	2	AAY14544	Aay14544	Mouse lip
20	2519.5	71.6	594	4	AAB59907	Aab59907	Murine le
21	2474.5	70.3	574	2	AAY14539	Aay14539	Rat lipol
22	2474.5	70.3	574	4	AAB59905	Aab59905	Rat lepti
23	2426	69.0	575	2	AAY14545	Aay14545	Mouse lip
24	2426	69.0	575	4	AAB59908	Aab59908	Murine le
25	2142	60.9	525	2	AAY14540	Aay14540	Rat lipol
26	2142	60.9	525	4	AAB59906	Aab59906	Rat lepti
27	2095.5	59.6	526	2	AAY14546	Aay14546	Mouse lip
28	2095.5	59.6	526	4	AAB59909	Aab59909	Murine le
29	1827.5	51.9	388	8	ADP46577	Adp46577	Human col
30	1138	32.3	208	8	ABO59373	Abo59373	Human gen
31	823.5	23.4	163	3	AAB53495	Aab53495	Human col
32	726	20.6	227	8	ADP46526	Adp46526	Human col
33	642.5	18.3	546	6	ABR43174	Abr43174	Human REM
34	638.5	18.1	540	8	ADR89882	Adr89882	FREP poly
35	637.5	18.1	635	8	ADR89880	Adr89880	FREP poly
36	502.5	14.3	265	7	ADM56943	Adm56943	Human cyt
37	465.5	13.2	241	7	ADM56944	Adm56944	Mature hu
38	452	12.8	428	4	AAU18010	Aau18010	Human imm
39	452	12.8	428	7	ADB31634	Adb31634	Human nov
40	452	12.8	430	4	ABB10256	Abb10256	Human cDN
41	452	12.8	430	5	ABP66843	Abp66843	Human pol
42	349	9.9	204	4	AAU18069	Aau18069	Human imm
43	349	9.9	204	4	ABB10461	Abb10461	Human cDN
44	349	9.9	204	5	ABP67048	Abp67048	Human pol
45	349	9.9	204	7	ADB31693	Adb31693	Human nov

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:18:25 ; Search time 51 Seconds
(without alignments)
1113.870 Million cell updates/sec

Title: US-10-650-507-8
Perfect score: 3518
Sequence: 1 MQQDGLGVGTRNGSGKGKRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3518	100.0	649	2	US-09-499-522-14	Sequence 14, Appl
2	3518	100.0	649	2	US-09-269-939A-8	Sequence 8, Appli
3	3401.5	96.7	630	2	US-09-499-522-16	Sequence 16, Appl
4	3401.5	96.7	630	2	US-09-269-939A-10	Sequence 10, Appl
5	3058	86.9	581	2	US-09-499-522-18	Sequence 18, Appl
6	3058	86.9	581	2	US-09-269-939A-12	Sequence 12, Appl
7	2568	73.0	593	2	US-09-269-939A-2	Sequence 2, Appli
8	2519.5	71.6	594	2	US-09-269-939A-16	Sequence 16, Appl

9	2474.5	70.3	574	2	US-09-269-939A-4	Sequence 4, Appli
10	2426	69.0	575	2	US-09-269-939A-17	Sequence 17, Appl
11	2142	60.9	525	2	US-09-269-939A-6	Sequence 6, Appli
12	2095.5	59.6	526	2	US-09-269-939A-18	Sequence 18, Appl
13	169.5	4.8	715	2	US-10-104-047-3385	Sequence 3385, Ap
14	166	4.7	977	2	US-09-252-991A-16655	Sequence 16655, A
15	153.5	4.4	437	2	US-09-538-092-876	Sequence 876, App
16	153.5	4.4	614	5	PCT-US95-03236-21	Sequence 21, Appl
17	153	4.3	316	2	US-09-397-243D-13	Sequence 13, Appl
18	150	4.3	767	2	US-09-252-991A-28262	Sequence 28262, A
19	150	4.3	1382	2	US-09-171-991-9	Sequence 9, Appli
20	150	4.3	1388	2	US-09-949-016-10817	Sequence 10817, A
21	148	4.2	1462	2	US-09-538-092-1043	Sequence 1043, Ap
22	148	4.2	1462	2	US-09-949-002-381	Sequence 381, App
23	148	4.2	1524	2	US-09-949-002-495	Sequence 495, App
24	146.5	4.2	777	2	US-09-252-991A-27864	Sequence 27864, A
25	146	4.2	998	2	US-09-949-016-7757	Sequence 7757, Ap
26	145.5	4.1	319	1	US-08-597-495B-22	Sequence 22, Appl
27	145.5	4.1	319	2	US-09-068-051A-22	Sequence 22, Appl
28	145.5	4.1	319	2	US-09-336-536-67	Sequence 67, Appl
29	145.5	4.1	319	2	US-09-254-465A-6	Sequence 6, Appli
30	145.5	4.1	319	2	US-09-953-499-6	Sequence 6, Appli
31	145.5	4.1	757	2	US-10-094-749-2685	Sequence 2685, Ap
32	144.5	4.1	691	2	US-09-252-991A-16809	Sequence 16809, A
33	144.5	4.1	783	2	US-09-252-991A-18035	Sequence 18035, A
34	143	4.1	636	2	US-09-252-991A-24902	Sequence 24902, A
35	143	4.1	743	2	US-09-902-540-10164	Sequence 10164, A
36	142.5	4.1	264	2	US-09-252-991A-20342	Sequence 20342, A
37	142	4.0	399	2	US-09-252-991A-25039	Sequence 25039, A
38	141.5	4.0	387	2	US-09-252-991A-30467	Sequence 30467, A
39	141	4.0	302	1	US-08-893-853-3	Sequence 3, Appli
40	141	4.0	302	2	US-09-113-921-3	Sequence 3, Appli
41	141	4.0	302	2	US-09-451-067-3	Sequence 3, Appli
42	141	4.0	302	3	US-10-086-208-3	Sequence 3, Appli
43	140	4.0	560	2	US-09-252-991A-26107	Sequence 26107, A
44	139.5	4.0	424	2	US-09-252-991A-22384	Sequence 22384, A
45	139	4.0	412	2	US-09-252-991A-23193	Sequence 23193, A

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:19:15 ; Search time 182 Seconds
(without alignments)
1651.794 Million cell updates/sec

Title: US-10-650-507-8
Perfect score: 3518
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3518	100.0	649	4	US-10-214-684A-14	Sequence 14, Appl
2	3518	100.0	649	4	US-10-650-507-8	Sequence 8, Appli
3	3518	100.0	649	6	US-11-236-198-3	Sequence 3, Appli
4	3401.5	96.7	630	4	US-10-214-684A-16	Sequence 16, Appl
5	3401.5	96.7	630	4	US-10-650-507-10	Sequence 10, Appl
6	3401.5	96.7	630	6	US-11-236-198-5	Sequence 5, Appli
7	3251	92.4	601	5	US-10-756-149-5066	Sequence 5066, Ap
8	3169	90.1	591	4	US-10-060-036-165	Sequence 165, App
9	3058	86.9	581	4	US-10-214-684A-18	Sequence 18, Appl
10	3058	86.9	581	4	US-10-650-507-12	Sequence 12, Appl

11	3058	86.9	581	6	US-11-236-198-7	Sequence 7, Appli
12	2568	73.0	593	4	US-10-650-507-2	Sequence 2, Appli
13	2568	73.0	593	6	US-11-236-198-9	Sequence 9, Appli
14	2519.5	71.6	594	4	US-10-650-507-16	Sequence 16, Appl
15	2519.5	71.6	594	6	US-11-236-198-17	Sequence 17, Appl
16	2474.5	70.3	574	4	US-10-650-507-4	Sequence 4, Appli
17	2474.5	70.3	574	6	US-11-236-198-11	Sequence 11, Appl
18	2426	69.0	575	4	US-10-650-507-17	Sequence 17, Appl
19	2426	69.0	575	6	US-11-236-198-18	Sequence 18, Appl
20	2142	60.9	525	4	US-10-650-507-6	Sequence 6, Appli
21	2142	60.9	525	6	US-11-236-198-13	Sequence 13, Appl
22	2095.5	59.6	526	4	US-10-650-507-18	Sequence 18, Appl
23	2095.5	59.6	526	6	US-11-236-198-19	Sequence 19, Appl
24	1138	32.3	208	4	US-10-029-386-33007	Sequence 33007, A
25	823.5	23.4	163	3	US-09-925-299-1035	Sequence 1035, Ap
26	823.5	23.4	163	3	US-09-925-299-1035	Sequence 1035, Ap
27	452	12.8	428	4	US-10-091-438-155	Sequence 155, App
28	452	12.8	430	3	US-09-764-853-564	Sequence 564, App
29	349	9.9	204	3	US-09-764-853-769	Sequence 769, App
30	349	9.9	204	4	US-10-091-438-214	Sequence 214, App
31	325	9.2	175	4	US-10-264-237-2542	Sequence 2542, Ap
32	251.5	7.1	138	4	US-10-029-386-29424	Sequence 29424, A
33	249.5	7.1	124	3	US-09-864-761-48029	Sequence 48029, A
34	233.5	6.6	110	3	US-09-864-761-37731	Sequence 37731, A
35	185	5.3	2263	4	US-10-408-765A-2231	Sequence 2231, Ap
36	185	5.3	2296	5	US-10-696-909A-46	Sequence 46, Appl
37	185	5.3	2752	5	US-10-696-909A-44	Sequence 44, Appl
38	169.5	4.8	715	4	US-10-104-047-3385	Sequence 3385, Ap
39	169.5	4.8	715	6	US-11-072-512-3385	Sequence 3385, Ap
40	166	4.7	448	6	US-11-097-143-8784	Sequence 8784, Ap
41	166	4.7	19652	4	US-10-084-846A-7	Sequence 7, Appli
42	163	4.6	1231	6	US-11-097-143-6006	Sequence 6006, Ap
43	162.5	4.6	505	4	US-10-264-049-3123	Sequence 3123, Ap
44	162	4.6	272	4	US-10-767-701-41627	Sequence 41627, A
45	161.5	4.6	1243	5	US-10-450-763-51580	Sequence 51580, A

This page gives you Search Results detail for the Application 10650507 and Search Result \$itemName.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:20:10 ; Search time 16 Seconds
(without alignments)
512.840 Million cell updates/sec

Title: US-10-650-507-8
Perfect score: 3518
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	152.5	4.3	655	7	US-11-293-697-2723 Sequence 2723, Ap
2	148	4.2	374	6	US-10-953-349-33957 Sequence 33957, A
3	146.5	4.2	347	6	US-10-953-349-3425 Sequence 3425, Ap
4	136	3.9	407	6	US-10-953-349-24955 Sequence 24955, A
5	136	3.9	471	6	US-10-953-349-24954 Sequence 24954, A
6	136	3.9	482	6	US-10-953-349-24953 Sequence 24953, A
7	133.5	3.8	523	6	US-10-953-349-35575 Sequence 35575, A
8	133	3.8	318	6	US-10-953-349-27945 Sequence 27945, A

9	133	3.8	343	6	US-10-953-349-27944	Sequence 27944, A
10	133	3.8	394	6	US-10-953-349-27943	Sequence 27943, A
11	132.5	3.8	377	6	US-10-953-349-35827	Sequence 35827, A
12	132	3.8	288	6	US-10-953-349-17941	Sequence 17941, A
13	132	3.8	834	6	US-10-953-349-9789	Sequence 9789, Ap
14	132	3.8	854	6	US-10-953-349-9788	Sequence 9788, Ap
15	132	3.8	878	6	US-10-953-349-9787	Sequence 9787, Ap
16	128.5	3.7	448	7	US-11-293-697-4755	Sequence 4755, Ap
17	127.5	3.6	353	6	US-10-953-349-35828	Sequence 35828, A
18	127.5	3.6	1460	7	US-11-247-437-14	Sequence 14, Appl
19	127	3.6	322	6	US-10-953-349-21883	Sequence 21883, A
20	125.5	3.6	382	6	US-10-953-349-2030	Sequence 2030, Ap
21	124.5	3.5	1935	6	US-10-480-962-6	Sequence 6, Appli
22	123.5	3.5	303	6	US-10-953-349-5570	Sequence 5570, Ap
23	123	3.5	671	6	US-10-196-749-346	Sequence 346, App
24	122.5	3.5	303	6	US-10-953-349-266	Sequence 266, App
25	121	3.4	596	6	US-10-953-349-35610	Sequence 35610, A
26	120	3.4	352	6	US-10-953-349-2031	Sequence 2031, Ap
27	118.5	3.4	542	7	US-11-293-697-4713	Sequence 4713, Ap
28	118	3.4	261	6	US-10-953-349-35829	Sequence 35829, A
29	117.5	3.3	363	6	US-10-953-349-24729	Sequence 24729, A
30	117.5	3.3	400	6	US-10-953-349-24728	Sequence 24728, A
31	117.5	3.3	583	6	US-10-953-349-35611	Sequence 35611, A
32	117	3.3	422	6	US-10-953-349-24756	Sequence 24756, A
33	117	3.3	458	6	US-10-953-349-24755	Sequence 24755, A
34	117	3.3	1023	7	US-11-293-697-3123	Sequence 3123, Ap
35	116	3.3	286	6	US-10-953-349-24757	Sequence 24757, A
36	115	3.3	390	6	US-10-953-349-22063	Sequence 22063, A
37	114.5	3.3	611	7	US-11-321-421-81	Sequence 81, Appl
38	114	3.2	310	6	US-10-953-349-12367	Sequence 12367, A
39	114	3.2	632	7	US-11-293-697-3548	Sequence 3548, Ap
40	113	3.2	621	7	US-11-293-697-3069	Sequence 3069, Ap
41	112.5	3.2	333	6	US-10-953-349-24730	Sequence 24730, A
42	112.5	3.2	373	6	US-10-953-349-31149	Sequence 31149, A
43	112.5	3.2	1126	7	US-11-293-697-3665	Sequence 3665, Ap
44	112	3.2	949	7	US-11-293-697-3033	Sequence 3033, Ap
45	111	3.2	237	6	US-10-953-349-27001	Sequence 27001, A

This page gives you Search Results detail for the Application 10650507 and Search Result us-10-650-507-8.rpr.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:13:19 ; Search time 44 Seconds
(without alignments)
1419.197 Million cell updates/sec

Title: US-10-650-507-8
Perfect score: 3518
Sequence: 1 MQQDGLGVGTRNGSGKGKRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	4.8	1173	2	T31421	C-terminal domain-
2	166	4.7	448	2	A36311	70K U1 small nucle
3	153.5	4.4	614	2	A25707	U1 snRNP 70K prote
4	149.5	4.2	1344	2	T42637	hypothetical prote
5	148	4.2	1403	1	A47328	natural killer cel
6	146.5	4.2	347	2	T08954	hypothetical prote
7	145	4.1	3942	2	T42730	Bassoon protein -
8	144.5	4.1	378	2	S04336	U1 snRNP 70K prote
9	144.5	4.1	670	2	T49510	fibroin-3 related
10	144.5	4.1	3938	2	T42761	Bassoon protein -
11	143.5	4.1	998	2	T30930	hypothetical prote
12	143.5	4.1	2022	2	T48818	glucan 1,4-alpha-g

13	143	4.1	2212	2	A41098	calcium channel pr
14	142.5	4.1	834	2	T42702	hypothetical prote
15	142	4.0	632	2	T02627	hypothetical prote
16	142	4.0	1208	2	T23467	hypothetical prote
17	141.5	4.0	948	2	A57640	retinoblastoma bin
18	141.5	4.0	963	2	T19140	hypothetical prote
19	141	4.0	2649	2	T51023	hypothetical prote
20	140.5	4.0	604	2	T37994	probable splicing
21	140	4.0	344	2	S59043	splicing factor SR
22	139.5	4.0	370	2	A87358	hypothetical prote
23	139.5	4.0	618	2	T42664	hypothetical prote
24	139	4.0	1571	2	T00062	hypothetical prote
25	138.5	3.9	335	2	T21503	hypothetical prote
26	138.5	3.9	489	2	A45988	dentin matrix acid
27	138	3.9	1888	2	S78476	collagen alpha 1(X
28	136	3.9	3124	2	A40020	collagen alpha 1(X
29	135	3.8	1870	2	S37671	MHC class III hist
30	134	3.8	309	2	T47685	probable RNA bindi
31	134	3.8	1097	2	T13033	cyclin T - fruit f
32	133.5	3.8	771	2	T21633	hypothetical prote
33	133.5	3.8	868	2	JC5701	ErbB kinase activa
34	133.5	3.8	2142	2	B35098	MHC class III hist
35	133	3.8	375	2	A40112	MHC-region RD-repe
36	132.5	3.8	287	2	T50647	serine/arginine-ri
37	132.5	3.8	374	2	A37282	52K active chromat
38	132.5	3.8	825	1	EDBEXD	immediate-early pr
39	132.5	3.8	1520	2	T00273	hypothetical prote
40	132.5	3.8	2774	2	A43359	microtubule-associ
41	132	3.8	309	2	A39773	myristylated alani
42	132	3.8	562	2	T26242	hypothetical prote
43	132	3.8	611	1	S12566	translation initia
44	132	3.8	725	2	T00492	hypothetical prote
45	131.5	3.7	697	2	JC2365	fused proteinase-c

This page gives you Search Results detail for the Application 10650507 and Search Result us-10-650-507-8.rup.

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OM protein - protein search, using sw model

Run on: June 9, 2006, 19:09:44 ; Search time 303 Seconds
(without alignments)
1981.304 Million cell updates/sec

Title: US-10-650-507-8
Perfect score: 3518
Sequence: 1 MQQDGLGVGTRNGSGKGRSV.....ASRERRLKKNLALSRESLVV 649

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3518	100.0	649	2	Q86X29_HUMAN	Q86x29 homo sapien
2	3372.5	95.9	630	2	Q6ZT80_HUMAN	Q6zt80 homo sapien
3	3169	90.1	591	2	Q9UQL3_HUMAN	Q9uql3 homo sapien
4	3124	88.8	583	2	Q9BT33_HUMAN	Q9bt33 homo sapien
5	3121	88.7	583	2	Q8NBM0_HUMAN	Q8nbm0 homo sapien
6	3116	88.6	582	2	Q9BWS2_HUMAN	Q9bws2 homo sapien
7	2619.5	74.5	656	2	Q61148_MOUSE	Q61148 mus musculu
8	2568	73.0	593	2	Q9WU74_RAT	Q9wu74 rattus norv
9	2526.5	71.8	594	2	Q99KG5_MOUSE	Q99kg5 mus musculu
10	2474.5	70.3	574	2	Q9WU75_RAT	Q9wu75 rattus norv
11	2470.5	70.2	574	2	Q497B9_RAT	Q497b9 rattus norv
12	2446.5	69.5	576	2	Q6U816_MOUSE	Q6u816 mus musculu
13	2433	69.2	575	2	Q3UIQ9_MOUSE	Q3uiq9 mus musculu
14	2304	65.5	429	2	O00112_HUMAN	O00112 homo sapien

15	2142	60.9	525	2	Q9WU76_RAT	Q9wu76	rattus norv
16	2093.5	59.5	526	2	Q3TJE7_MOUSE	Q3tje7	mus musculu
17	1554.5	44.2	575	2	Q6GPK3_XENLA	Q6gpk3	xenopus lae
18	1460.5	41.5	270	2	O00426_HUMAN	O00426	homo sapien
19	1340	38.1	248	2	Q499Z8_HUMAN	Q499z8	homo sapien
20	1331	37.8	339	2	Q61149_MOUSE	Q61149	mus musculu
21	1174.5	33.4	638	2	Q6GMG1_BRARE	Q6gmg1	brachydanio
22	1159	32.9	594	2	Q4V8Y3_BRARE	Q4v8y3	brachydanio
23	965	27.4	639	2	Q71H61_HUMAN	Q71h61	homo sapien
24	722.5	20.5	663	2	Q4SHQ6_TETNG	Q4shq6	tetraodon n
25	715.5	20.3	557	2	Q4KMJ6_BRARE	Q4kmj6	brachydanio
26	676.5	19.2	194	2	Q4T5P9_TETNG	Q4t5p9	tetraodon n
27	634.5	18.0	546	2	Q5R8C7_PONPY	Q5r8c7	pongo pygma
28	616.5	17.5	502	2	Q86SU0_HUMAN	Q86su0	homo sapien
29	608.5	17.3	537	2	Q8CBR1_MOUSE	Q8cbr1	mus musculu
30	607.5	17.3	545	2	Q32NM7_XENLA	Q32nm7	xenopus lae
31	598.5	17.0	516	2	Q91VS0_MOUSE	Q91vs0	mus musculu
32	595.5	16.9	493	2	Q6PFB3_MOUSE	Q6pfb3	mus musculu
33	595.5	16.9	516	2	Q8CB39_MOUSE	Q8cb39	mus musculu
34	556.5	15.8	550	2	Q66L52_BRARE	Q66l52	brachydanio
35	548	15.6	573	2	Q4S0L1_TETNG	Q4s0l1	tetraodon n
36	547.5	15.6	464	2	Q7T2Z9_BRARE	Q7t2z9	brachydanio
37	545	15.5	470	2	Q4SHT3_TETNG	Q4sht3	tetraodon n
38	506	14.4	559	2	Q4S0L2_TETNG	Q4s0l2	tetraodon n
39	502.5	14.3	265	2	Q7Z578_HUMAN	Q7z578	homo sapien
40	190.5	5.4	96	2	Q4T5Q0_TETNG	Q4t5q0	tetraodon n
41	188	5.3	836	2	Q4WU48_ASPFU	Q4wu48	aspergillus
42	185	5.3	956	2	Q9UQ39_HUMAN	Q9uq39	homo sapien
43	185	5.3	1022	2	Q6NSL3_HUMAN	Q6nsl3	homo sapien
44	185	5.3	1262	2	Q9UQ40_HUMAN	Q9uq40	homo sapien
45	185	5.3	2296	2	Q9UHA8_HUMAN	Q9uha8	homo sapien